Dysferlin is a complex, multi-C2-domain protein whose functions include membrane fusion and membrane repair. Progress in studying the domain composition of dysferlin has been problematic due to its large size and the difficulty in computing accurate residue ranges for each respective dysferlin protein domain. However, recent advances in in silico protein folding methods have significantly enhanced the understanding of the domain structure of these complex proteins. To compute unbiased domain boundaries of the complete dysferlin protein, we used RoseTTAFold to assemble full-length models for each of the six human ferlin proteins (dysferlin, myoferlin, otoferlin, Fer1L4, Fer1L5, and Fer1L6). The RoseTTAFold/AlphaFold2 in silico boundary prediction methods allowed us to describe and characterize a previously unknown C2 domain, which we refer to as C2-FerA. At present, the dysferlin domain-domain interactions implied by the full-length in silico models are predicted to have a low accuracy; however, the use of RoseTTAFold and AlphaFold2 as a domain finder has proven to be a powerful research tool in understanding dysferlin structure.